

## **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/539,954  
Source: PTI/10  
Date Processed by STIC: 6/30/05

***ENTERED***



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/539,954

DATE: 06/30/2005

TIME: 09:07:41

Input Set : A:\Final sequence list-13195-00006-US.txt  
 Output Set: N:\CRF4\06302005\J539954.raw

3 <110> APPLICANT: Schmitz, Oliver  
 4 Puzio, Piotr  
 5 Blau, Astrid  
 6 Looser, Ralf  
 7 Wendel, Birgit  
 8 Kamlage, Beate  
 9 Plesch, Gunnar  
 11 <120> TITLE OF INVENTION: Method for Producing Amino Acids  
 13 <130> FILE REFERENCE: 13195-00006-US  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/539,954  
 C--> 15 <141> CURRENT FILING DATE: 2005-06-17  
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014649  
 16 <151> PRIOR FILING DATE: 2003-12-19  
 18 <150> PRIOR APPLICATION NUMBER: DE 102 61 188.2  
 19 <151> PRIOR FILING DATE: 2002-12-20  
 21 <160> NUMBER OF SEQ ID NOS: 26  
 23 <170> SOFTWARE: PatentIn version 3.3  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 1164  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Saccharomyces cerevisiae  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (1)..(1164)  
 34 <223> OTHER INFORMATION: Threonine aldolase  
 36 <400> SEQUENCE: 1  
 37 atg act gaa ttc gaa ttg cct cca aaa tat atc acc gct gct aac gac 48  
 38 Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp  
 39 1 5 10 15  
 41 ttg cgg tca gac aca ttc acc act cca act gca gag atg atg gag gcc 96  
 42 Leu Arg Ser Asp Thr Phe Thr Pro Thr Ala Glu Met Met Glu Ala  
 43 20 25 30  
 45 gct tta gag gcc tct atc ggt gac gct gtc tac ggt gaa gat gtt gac 144  
 46 Ala Leu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp  
 47 35 40 45  
 49 acc gtt agg ctc gaa cag acc gtt gcc cgc atg gct ggc aaa gaa gca 192  
 50 Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala  
 51 50 55 60  
 53 ggt ttg ttc tgt gtc tct qgg act ttg tcc aac cag att gcc atc aga 240  
 54 Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg  
 55 65 70 75 80  
 57 act cac ttg atg caa cct cca tac tct att cta tgt gat tac agg gct 288  
 58 Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala

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**Input Set : A:\Final sequence list-13195-00006-US.txt**  
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59	85	90	95	
61	cac gtt tac act cac gaa gcc gct gga ctg gcg atc ttg tct caa gcg			336
62	His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala			
63	100	105	110	
65	atg gtg gtt cct gtg gtt cct tcc aac ggt gac tac ttg acc ttg gaa			384
66	Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu			
67	115	120	125	
69	gac atc aag tca cac tac gtc cca gac gac ggt gat att cac ggt gcc			432
70	Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala			
71	130	135	140	
73	ccc acc aga ttg att tct ctg gaa aac act tta cac ggt att gtt tat			480
74	Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr			
75	145	150	155	160
77	cca ttg gaa gaa ctg gtc cgc atc aaa gct tgg tgt atg gaa aat ggt			528
78	Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly			
79	165	170	175	
81	ctc aaa cta cat tgt gac ggt gcc aga atc tgg aat gcc gct gca caa			576
82	Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Gln			
83	180	185	190	
85	tct ggc gtg cca tta aag caa tat ggg gaa atc ttc gac tcc atc tcc			624
86	Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser			
87	195	200	205	
89	atc tgt cta tcc aag tct atg ggt gct cct att ggg tcc gtc ttg gtt			672
90	Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val			
91	210	215	220	
93	ggg aac ctt aag ttt gtc aag aag gcc acc cat ttc aga aaa caa caa			720
94	Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln			
95	225	230	235	240
97	ggt ggt att aga caa tct ggt atg atg gct aga atg gct ctt gta			768
98	Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val			
99	245	250	255	
101	aac atc aac aac gat tgg aag tcc caa ttg ctg tac tcg cac tct ttg			816
102	Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu			
103	260	265	270	
105	gct cat gaa tta gcc gaa tat tgt gag gca aag ggc atc ccg cta gag			864
106	Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu			
107	275	280	285	
109	tct cca gca gac acc aac ttt gtc ttt att aac ctg aag gcc gct aga			912
110	Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg			
111	290	295	300	
113	atg gac cca gat gtc ctt gtt aag aag ggt ttg aag tac aac gtt aag			960
114	Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys			
115	305	310	315	320
117	cta atg ggt ggt aga gtc tcg ttc cac tat caa gtc acc aga gat act			1008
118	Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr			
119	325	330	335	
121	ttg gaa aaa gtc aaa ttg gcc atc tcc gag gcc ttc gac tat gct aaa			1056
122	Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys			
123	340	345	350	

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125 gaa cat cct ttc gac tgt aac gga cct acc cag att tac cgt agt gaa      1104
126 Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu
127          355           360           365
129 tcc acc gag gtc gac gtt gat ggc aac gct atc cgc gaa ata aaa acc      1152
130 Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr
131          370           375           380
133 tac aaa tac tga
134 Tyr Lys Tyr
135 385
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 387
140 <212> TYPE: PRT
141 <213> ORGANISM: Saccharomyces cerevisiae
143 <400> SEQUENCE: 2
144 Met Thr Glu Phe Glu Leu Pro Pro Lys Tyr Ile Thr Ala Ala Asn Asp
145 1          5           10           15
147 Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala
148          20          25           30
150 Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp
151          35          40           45
153 Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala
154          50          55           60
156 Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg
157 65          70           75           80
159 Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala
160          85          90           95
162 His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala
163          100         105          110
165 Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu
166          115         120          125
168 Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala
169          130         135          140
171 Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr
172 145          150         155          160
174 Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly
175          165         170          175
177 Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Gln
178          180         185          190
180 Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser
181          195         200          205
183 Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val
184          210         215          220
186 Gly Asn Leu Lys Phe Val Lys Ala Thr His Phe Arg Lys Gln Gln
187 225          230         235          240
189 Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val
190          245         250          255
192 Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu
193          260         265          270
195 Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu

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**Output Set: N:\CRF4\06302005\J539954.raw**

196	275	280	285	
198	Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg			
199	290	295	300	
201	Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys			
202	305	310	315	320
204	Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr			
205	325	330	335	
207	Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys			
208	340	345	350	
210	Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu			
211	355	360	365	
213	Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr			
214	370	375	380	
216	Tyr Lys Tyr			
217	385			
220	<210> SEQ ID NO: 3			
221	<211> LENGTH: 376			
222	<212> TYPE: PRT			
223	<213> ORGANISM: Canola			
225	<400> SEQUENCE: 3			
226	Gly Cys Phe Ala Cys Tyr Leu Val Gly Gly Phe Ser Val Gln Glu Lys			
227	1	5	10	15
229	Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro			
230	20	25	30	
232	Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp			
233	35	40	45	
235	Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala			
236	50	55	60	
239	Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met			
240	65	70	75	80
242	Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu			
243	85	90	95	
245	Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly			
246	100	105	110	
248	Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp			
249	115	120	125	
251	Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro			
252	130	135	140	
254	Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn			
255	145	150	155	160
257	Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp			
258	165	170	175	
260	Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp			
261	180	185	190	
263	Gly Ala Arg Ile Phe Asn Ala Ser Val Ala Leu Gly Val Pro Val Asp			
264	195	200	205	
266	Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly			
267	210	215	220	
269	Ile Gly Ala Pro Val Gly Ser Val Ile Val Gly Ser Lys Asn Phe Ile			

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270 225          230          235          240
272 Ala Lys Ala Arg Arg Leu Arg Lys Thr Leu Gly Gly Met Arg Gln
273          245          250          255
275 Ile Gly Leu Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Val
276          260          265          270
278 Gly Lys Leu Glu Ser Asp His Lys Lys Ala Arg Leu Leu Ala Asp Gly
279          275          280          285
281 Leu Asn Glu Val Lys Gly Leu Arg Val Asp Ala Cys Ser Val Glu Thr
282          290          295          300
284 Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu
285 305          310          315          320
287 Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu
288          325          330          335
290 Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser
291          340          345          350
293 Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys
294          355          360          365
296 Gly Val Gln Lys Glu Met Gly Asn
297          370          375
300 <210> SEQ ID NO: 4
301 <211> LENGTH: 115
302 <212> TYPE: PRT
303 <213> ORGANISM: Soybean
305 <400> SEQUENCE: 4
306 Leu Phe Gly Leu Leu Ala Ile Leu Leu Glu Tyr Leu Glu Lys Met Val
307 1          5          10          15
309 Pro Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro Ser Glu
310          20          25          30
312 Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp Val Leu
313          35          40          45
315 Gly Arg Asp Pro Ser Cys Phe Arg Leu Glu Thr Glu Met Ala Lys Ile
316          50          55          60
318 Leu Gly Lys Glu Gly Ala Leu Phe Val Pro Ser Gly Thr Met Ala Asn
319 65          70          75          80
321 Leu Ile Ser Val Leu Val His Cys Asp Ile Arg Gly Ser Glu Val Ile
322          85          90          95
324 Leu Gly Asp Asn Ser His Ile His Ile Tyr Glu Asn Gly Gly Ile Ala
325          100         105         110
327 Thr Leu Gly
328          115
331 <210> SEQ ID NO: 5
332 <211> LENGTH: 127
333 <212> TYPE: PRT
334 <213> ORGANISM: Rice
336 <220> FEATURE:
337 <221> NAME/KEY: misc_feature
338 <222> LOCATION: (1)..(127)
339 <223> OTHER INFORMATION: unknown or other
341 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY                   DATE: 06/30/2005  
PATENT APPLICATION: US/10/539,954                   TIME: 09:07:42

Input Set : A:\Final sequence list-13195-00006-US.txt  
Output Set: N:\CRF4\06302005\J539954.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 4  
Seq#:7; Xaa Pos. 5

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/539,954

DATE: 06/30/2005

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Input Set : A:\Final sequence list-13195-00006-US.txt  
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L:15 M:270 C: Current Application Number differs, Replaced Current Application No  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0